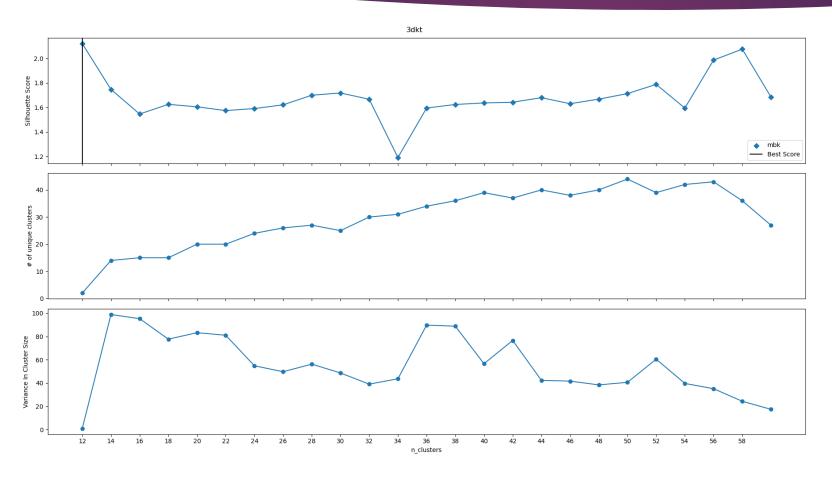
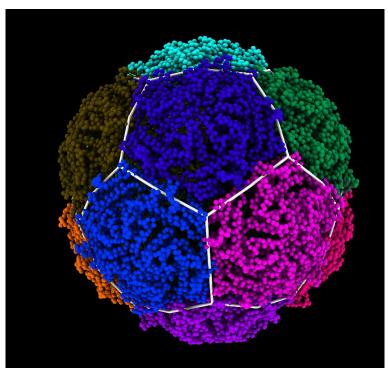
HK97 Results

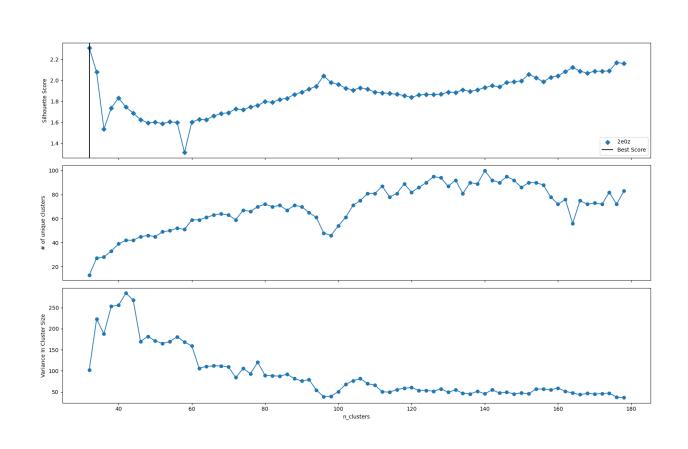
Thermotoga Maritima Encapsulin (3dkt)

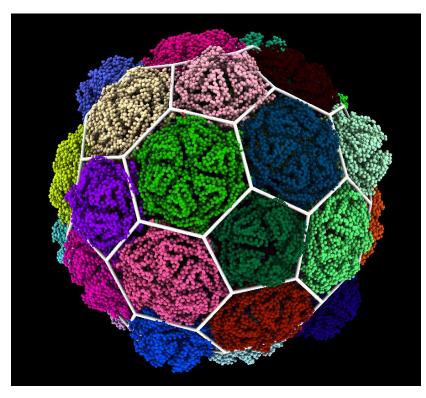




T=1 Hexagonal

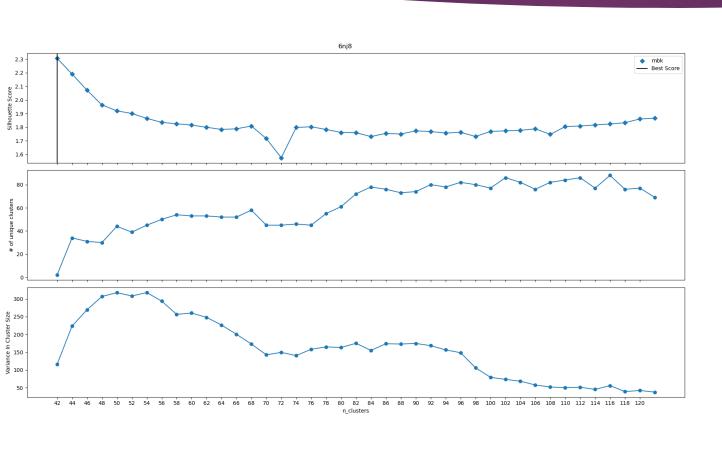
VLP From Pyrococcus Furiosus (2e0z)

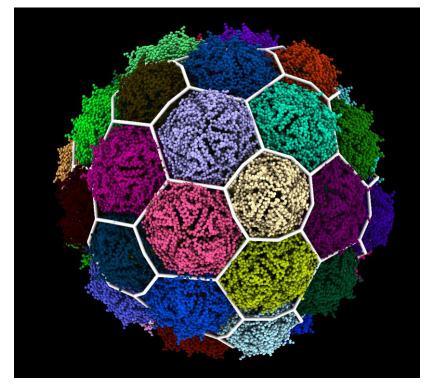




T=3 Hexagonal

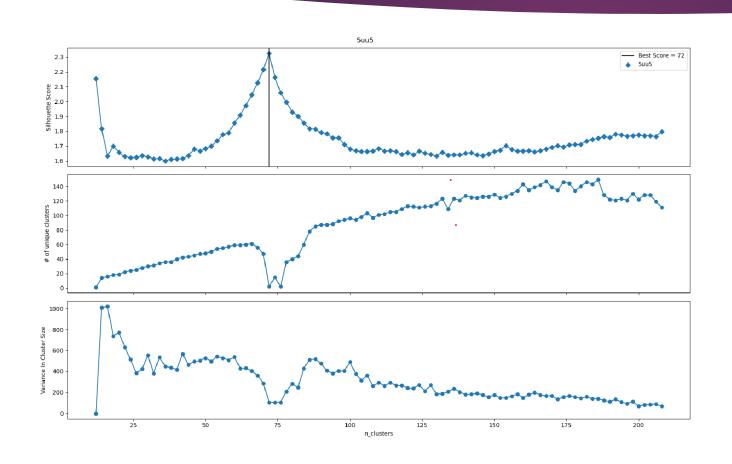
Iron Storage Encapsulin From Quasibacillus thermotolerans (6nj8)

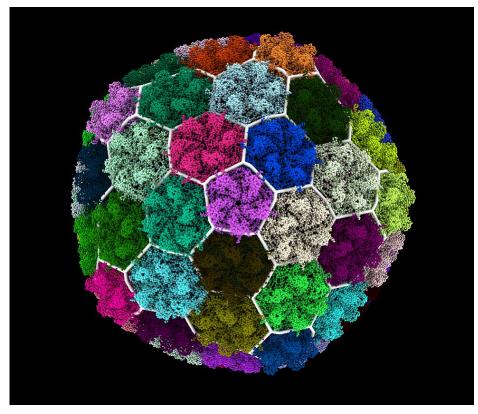




T=3 Hexagonal

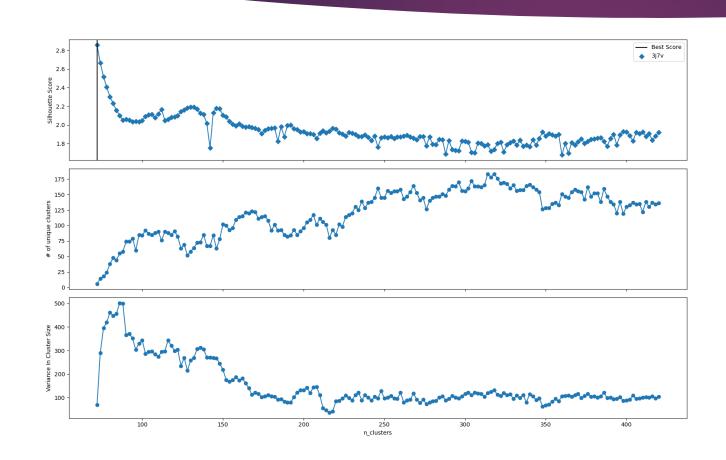
Bacteriopohage P22 Mature Virion (5uu5)

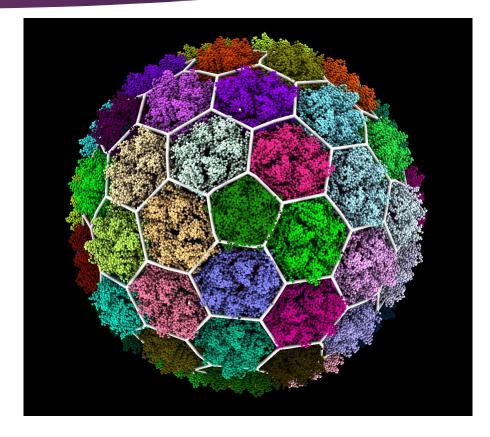




T=7 Hexagonal

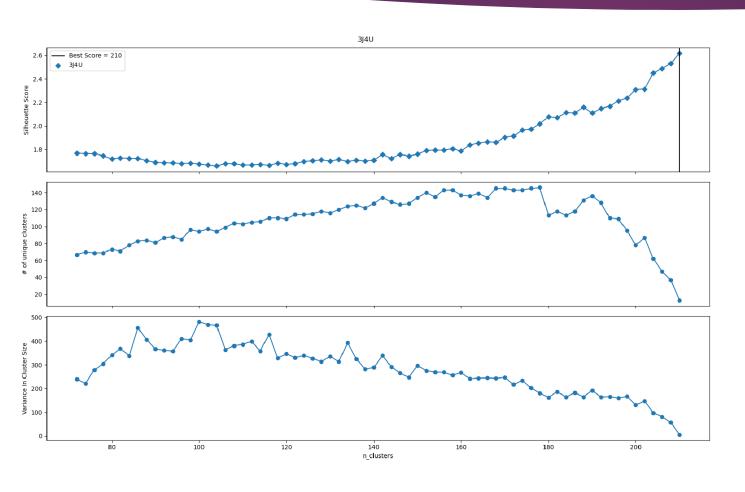
Bacteriopohage T7 Procapsid (3j7v)

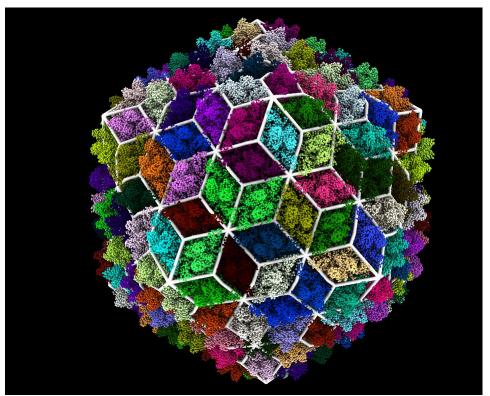




T=7 Hexagonal

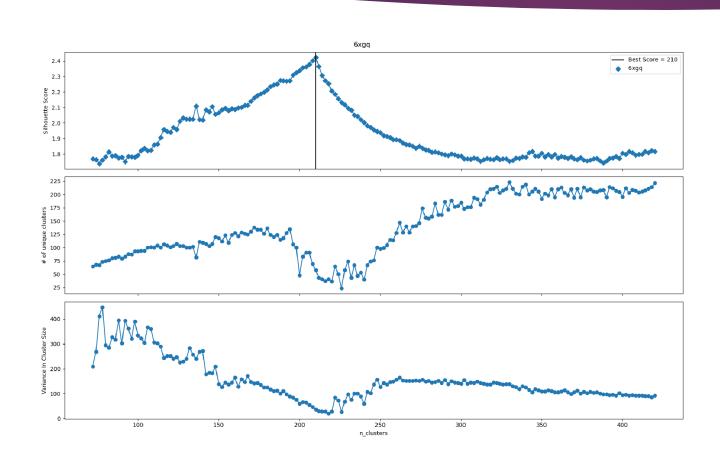
Bordetella Bacteriophage (3j4u)

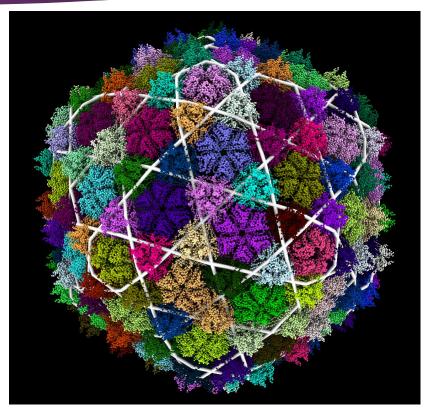




T=7 Trihexagonal-Dual (Imperfect Subdivision)

YSD1 Bacteriophage (6xgq)





T=7 Trihexagonal (Imperfect Subdivision)

Discussion

- ▶ P22 lacked reinforcement proteins and was labelled as hexagonal
- Bordetella and Phage YSD1 had reinforcement proteins around the local 2-fold and 3-fold axes respectively and were labeled as trihex-dual and trihex.
- ► This suggests the presence and location of reinforcement proteins could determine lattice structure.
- ▶ Both Bordatella and YSD1 had error in their label assignments. The tool becomes less accurate at a large number of clusters.